

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 27, 2002, 03:36:38 : Search time 1259.04 Seconds

(without alignments)
7350.398 Million cell updates/sec

Title: US-09-893-615-88

Perfect score: 318
Sequence: 1 CAATTGTCCTCCAGTC.....GGACCAGCTGGAATATAGA 318Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 1451402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vi:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pin:*
35: em.htg.tod:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303.6	95.5	321	10 MMIG013	X58586 Mouse hybr
2	301.6	94.8	318	10 AF178620	AF178620 Mus muscu
3	301	94.7	318	10 AF178619	AF178619 Mus muscu
4	300.4	94.5	321	6 AR096128	AR096128 Sequence
5	300.4	94.5	321	6 AR210527	AR210527 Sequence
6	300.4	94.5	384	6 AR000010	AR000010 Sequence
7	300.4	94.5	384	6 AR060923	AR060923 Sequence
8	300.4	94.5	384	6 AR211055	AR211055 Sequence
9	300.4	94.5	384	6 AX032417	AX032417 Sequence
10	300.4	94.5	384	6 BD004717	BD004717 Chimeric
11	300.4	94.5	9209	6 AR000007	AR000007 Sequence
12	300.4	94.5	9209	6 AR060920	AR060920 Sequence
13	300.4	94.5	9209	6 AR211052	AR211052 Sequence
14	300.4	94.5	9209	6 AX032414	AX032414 Sequence
15	300.4	94.5	9209	6 BD004714	BD004714 Chimeric
16	300.4	94.5	18986	6 AR051652	AR051652 Sequence
17	300.4	94.5	18986	6 AR092290	AR092290 Sequence
18	298.8	94.0	384	6 AR015962	AR015962 Sequence
19	298.8	94.0	1370	10 MUSIGKAR	K01641 Mouse Ig ka
20	297.2	93.5	9209	6 AR015961	AR015961 Sequence
21	295.6	93.0	318	6 AR096196	AR096196 Sequence
22	295.6	93.0	318	6 AR210595	AR210595 Sequence
23	295.6	93.0	335	6 AR096195	AR096195 Sequence
24	295.6	93.0	335	6 AR210594	AR210594 Sequence
25	295.6	93.0	403	6 I09200	I09200 Sequence 40
26	295.6	93.0	403	10 MUSIGKCN	M17954 Mouse Ig re
27	295.6	92.5	477	10 S76823	S76823 Ig V kappa
28	294.2	92.5	345	10 MUSIGKYA2A	M97864 Mouse hybr
29	294	92.0	309	10 I05923	I05923 Sequence 39
30	292.6	92.0	309	10 MMIGVKP4	X06517 Mouse Ig ac
31	292.4	91.9	302	10 MUSIGKAF	M64153 Mus musculu
32	290.8	91.4	350	10 AY058906	AY058906 Mus muscu
33	290.8	91.4	384	10 MM005285	U05285 Mus musculu
34	290.8	91.4	403	6 I08812	I08812 Sequence 14
35	290.8	91.4	732	6 A51863	A51863 Sequence 27
36	290.8	91.4	732	6 A83237	A83237 Sequence 57
37	290.8	91.4	732	6 AR085831	AR085831 Sequence
38	290.8	91.4	732	6 AR182961	AR182961 Sequence
39	289.4	91.0	318	12 AF277092	AF277092 Synthetic
40	289.4	91.0	765	6 AX057984	AX057984 Sequence
41	289.4	91.0	1239	6 AX057945	AX057945 Sequence
42	289.4	91.0	1280	6 AX057947	AX057947 Sequence
43	288.2	90.6	435	6 A17967	A17967 Variable re
44	288	90.6	360	10 AF029237	AF029237 Mus muscu
45	287.6	90.4	705	6 A83197	AR3197 Sequence 17

ALIGNMENTS

RESULT 1
MMIG013 321 bp mRNA Direct ROD 06-ANG-1995
DEFINITION Mouse hybridoma 2d3 mRNA for immunoglobulin kappa light chain V
LOCUS X58586 Y00794
ACCESSION X58586.1 GI:51562
VERSION X58586.1
KEYWORDS Ig kappa light chain; Ig variable region; immunoglobulin.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 321)
AUTHORS Week, K.
TITLE Direct Submission

JOURNAL Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern Medical School, 5323 Harry Hines Blvd, Microbiology, Dallas Texas 75235, USA

REFERENCE 2 (bases 1 to 321)
Meek, K., Hasemann, C., Pollok, B., Alkan, S. S., Bralt, M., Slaoui, M., Urban, J. and Capra, J. D.
STRUCTURAL CHARACTERIZATION OF ANTIDIDIOTYPIC ANTIBODIES. EVIDENCE THAT AB28 ARE DERIVED FROM THE GERMLINE DIFFERENTLY THAN AB18

JOURNAL J. Exp. Med. 169 (2), 519-533 (1989)

MEDLINE 89094248

PUBMED 2492056

FEATURES

Location/Qualifiers

1..321

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/cell_line="Hybridoma 2D3-K"

1..321

/gene="Ig kappa light chain"

<1..>321

/gene="Ig kappa light chain"

/note="variable region"

/evidence="experimental"

<1..>321

/gene="Ig kappa light chain"

/note="variable region"

/codon_start=1

/product="Ig kappa light chain"

/protein_id="CA41461.1"

/db_xref="GI:938245"

/translation="QIVLSQSPALISASPEKVTMTCRASSVSVMYVQKPGSSPK PWIATSNLASGVPARFSGSGSTSYSLTISRVAEDATYYCHQMSNPTFGGTR LEIR"

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/gene="Ig kappa light chain"

/product="Ig kappa light chain"

/note="variable region"

V_region

BASE COUNT 78 a 92 c 80 g 71 t

ORIGIN

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Best Local Similarity 97.2%; Pred. No. 3.8e-90;
Matches 309; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

1 CAATGTTCTCTCCAGCTCCAGCAATCTCTGTCATCTCCAGGGAAGAAGTCACA 60
1 CAATGTTCTCTCCAGCTCCAGCAATCTCTGTCATCTCCAGGGAAGAAGTCACA 60

61 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGTGACGAGCAAGCCAGGA 120
61 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGTGACGAGCAAGCCAGGA 120

121 TCTCTCCCAAAACCTGGATTTTCGCCACATCCAACTGGCTTGTGAGTCCCTGCTCG 180
121 TCTCTCCCAAAACCTGGATTTTCGCCACATCCAACTGGCTTGTGAGTCCCTGCTCG 180

181 TTCAGTGCAGAGTGTGAGACCTCTACTCTCTCAACAATCAGACAGAGAGAGCTGA 240
181 TTCAGTGCAGAGTGTGAGACCTCTACTCTCTCAACAATCAGACAGAGAGAGCTGA 240

241 GATGTCGCACTTATTACTGCCAGAGTGAAGTAACCCACCACGTTGAGAGGGGG 300
241 GATGTCGCACTTATTACTGCCAGAGTGAAGTAACCCACCACGTTGAGAGGGGG 300

301 ACCATGCTGAATAAGA 318
301 ACCATGCTGAATAAGA 318

RESULT 2
AF178620 318 bp mRNA linear ROD 22-MAY-2000
LOCUS AF178620
DEFINITION Mus musculus 39-9 Immunoglobulin light chain variable region mRNA.

Partial cds.

ACCESSION AF178620
VERSION AF178620.1 GI:5853223

KEYWORDS Mus musculus.

SOURCE Mus musculus.

ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 318)
Puterman, C., Decocharan, B. and Diamond, B.
Molecular analysis of the autoantibody response in peptide-induced autoimmunity

JOURNAL J. Immunol. 164 (5), 2542-2549 (2000)

MEDLINE 20143847

PUBMED 10679092

REFERENCE 2 (bases 1 to 318)
Puterman, C., Decocharan, B. and Diamond, B.
Direct Submission
Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA

FEATURES

Location/Qualifiers

1..318

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/cell_line="39-9"

/cell_type="hybridoma"

/note="from peptide-immunized mouse"

<1..>318

/note="Ig kappa; anti-peptide antibody"

/codon_start=1

/product="Immunoglobulin light chain variable region"

/protein_id="AAD54373.1"

/db_xref="GI:5853224"

/translation="QIVLSQSPALISASPEKVTMTCRASSVSVMYVQKPGSSPK PWIATSNLASGVPARFSGSGSTSYSLTISRVAEDATYYCHQMSNPTFGGTR LEIR"

BASE COUNT 75 a 89 c 81 g 73 t

ORIGIN

Query Match 94.8%; Score 301.6; DB 10; Length 318;
Best Local Similarity 97.2%; Pred. No. 1.8e-89;
Matches 307; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

3 AATGTTCTCTCCAGCTCCAGCAATCTCTGTCATCTCCAGGGAAGAAGTCACA 62
3 AATGTTCTCTCCAGCTCCAGCAATCTCTGTCATCTCCAGGGAAGAAGTCACA 62

63 GACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGTGACGAGCAAGCCAGGATC 122
63 GACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGTGACGAGCAAGCCAGGATC 122

123 CTCCCAAAACCCGGATTTTCGCCACATCCAACTGGCTTGTGAGTCCCTGCTCG 182
123 CTCCCAAAACCCGGATTTTCGCCACATCCAACTGGCTTGTGAGTCCCTGCTCG 182

183 CAGTGCAGAGTGTGAGACCTCTACTCTCTCAACAATCAGACAGAGAGAGCTGA 242
183 CAGTGCAGAGTGTGAGACCTCTACTCTCTCAACAATCAGACAGAGAGAGCTGA 242

243 TGTGTCGCACTTATTACTGCCAGAGTGAAGTAACCCACCACGTTGAGAGGGGGAC 302
243 TGTGTCGCACTTATTACTGCCAGAGTGAAGTAACCCACCACGTTGAGAGGGGGAC 302

303 CATGCTGAATAAGA 318
303 CATGCTGAATAAGA 318

RESULT 3
AF178619 318 bp mRNA linear ROD 22-MAY-2000
LOCUS AF178619
DEFINITION Mus musculus 8-3 Immunoglobulin light chain variable region mRNA.